

AMENDMENTS TO THE SPECIFICATION

Please replace the current sequence listing in the application with the enclosed sequence listing.

Please amend the priority claim on page 1 of the application to read as follows.

This application claims priority from U.S. Serial No. 60/426,592, filed November 15, 2002, which is incorporated by reference herein in its entirety. This application also is a continuation-in-part of PCT international application PCT/US03/36623, filed November 13, 2003 (WO 2004/045529, published June 3, 2004).

Please amend the paragraph bridging pages 3 and 4 of the specification to include sequence identification numbers for West Nile virus strain NY99-flamingo 382-99, as follows.

In one example of a chimeric virus of the invention, the attenuating mutation is in the region of position 107, 316, or 440 (or a combination thereof) of the West Nile virus envelope protein. The mutations can thus be, for example, in one or more of amino acids 102-112, 311-321, and/or 435-445 of the West Nile envelope protein. As a specific example, using the sequence of West Nile virus strain NY99-flamingo 382-99 (GenBank Accession Number AF196835; SEQ ID NOs:8 (nucleic acid) and 9 (amino acid)) as a reference, lysine at position 107 can be replaced with phenylalanine, alanine at position 316 can be replaced with valine, and/or lysine at position 440 can be replaced with arginine. In addition to the amino acids noted above, the substitutions can be made with other amino acids, such as amino acids that would

result in a conservative change from those noted above. Conservative substitutions typically include substitutions within the following groups: glycine, alanine, valine, isoleucine, and leucine; aspartic acid, glutamic acid, asparagine, and glutamine; serine and threonine; lysine and arginine; and phenylalanine and tyrosine. In a specific example, a chimera of the invention includes each of the specific substitutions noted above. Further, as is discussed further below, additional residues (e.g., positions 138, 176, and/or 280) can also be altered in the chimeric viruses of the present invention.

Please amend Table 1, on page 12 of the specification, to include sequence identification numbers, as follows.

Table 1
Switch Oligonucleotides used for site-mutagenesis

<u>E Protein</u> <u>position and</u> <u>residue</u>	Primer	Marker Site
107 L→F	5' CAACg ^{g} CTgC ^{g} gATTTTTTgCAA ^{g} gATCCATTgACACATgCgCC 3' (SEQ ID NO:1)	<i>Bam</i> HI
138 E→K	5' gAAAgAgAATATTAAgTACAAAgTggCCATTTTTgTCC 3' (SEQ ID NO:2)	<i>Ssp</i> I
*176 V	5' gCCCTCgAgCggCCgATTCAgCATCACTCCTgCTgCgCCTTCAgTCACAC 3' (SEQ ID NO:3)	
*176 Y	5' gCCCTCgAgCggCCgATTCAgCATCAC-3' (SEQ ID NO:4)	
280 K→M	5'-gCAACACTgTCATgTTAACgTCgggTCATTTg 3' (SEQ ID NO:5)	<i>Hpa</i> I
316 A→V	5'-CTTgggACTCCCgTggACACcgTCACggCAC-3' (SEQ ID NO:6)	<i>Age</i> I
440 K→R	5'-ggggTgTTCACTAgTgTTgggCgggCTgTCCATCAAgTg-3' (SEQ ID NO:7)	<i>Spe</i> I

Primers for site-directed mutagenesis to create mutant attenuated Yellow Fever/West Nile Virus. Nucleotide changes that introduce a new amino acid are indicated in bold. Silent restriction sites introduced are underlined. Primers indicated with an * (asterisk) are cloning primers used to sub-clone the fragment. One incorporates a nucleotide change while the other does not.